Rec'd POT/PTS 03 MAY 2005

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH <120> NUCLEOTIDE SEQUENCES THAT ENCODE CORYNEFORM BACTERIA FOR PROTEINS PARTICIPATING IN THE BIOSYNTHESIS OF L-SERINE AND METHOD OF PRODUCING L-SERINE <130> 23155 <140> <141> <160> 19 <170> PatentIn Ver. 2.1 <210> 1 <211> 1253 <212> DNA <213> Corynebacterium glutamicum <400> 1 totagagoog gagaogtgaa taaaattogo agotoattoo atcagogtaa acqoaqottt 60 ttgcatggtg agacaccttt gggggtaaat ctcacagcat gaatctctgg gttagatgac 120 tttctgggtg ggggagggtt tagaatgttt ctagtcgcac gccaaaaccc ggcgtggaca 180 cgtctgcagc cgacgcggtc gtgcctgttg tagacggaca ttcctagttt ttccaggagt 240 aacttgtgag ccagaatggc cgtccggtag tcctcatcgc cgataagctt gcgcagtcca 300 ctgttgacgc gcttggagat gcagtagaag tccgttgggt tgacggacct aaccgcccag 360 aactgcttga tgcagttaag gaagcggacg cactgctcgt gcgttctgct accactgtcg 420 atgetgaagt categeeget geeectaact tgaagategt eggtegtgee ggegtggget 480 tggacaacgt tgacatccct gctgccactg aagctggcgt catggttgct aacgcaccga 540 cctctaatat tcactccgct tgtgagcacg caatttcttt gctgctgtct actgctcgcc 600 agatecetge tgetgatgeg aegetgegtg agggegagtg gaageggtet tettteaaeg 660 gtgtggaaat tttcggaaaa actgtcggta tcgtcggttt tggccacatt ggtcagttgt 720 ttgctcagcg tcttgctgcg tttgagacca ccattgttgc ttacgatcct tacgctaacc 780 ctgctcgtgc ggctcagctg aacgttgagt tggttgagtt ggatgagctg atgagccgtt 840 ctgactttgt caccattcac cttcctaaga ccaaggaaac tgctggcatg tttgatgcgc 900 ageteettge taagteeaag aagggeeaga teateateaa egetgetegt ggtggeettg 960 ttgatgagca ggctttggct gatgcgattg agtccggtca cattcgtggc gctggtttcg 1020 atgtgtactc caccgagect tgcactgatt ctcetttgtt caagttgeet caggttgttg 1080 tgactcctca cttgggtgct tctactgaag aggctcagga tcgtgcgggt actgacgttg 1140 ctgattctgt gctcaaggcg ctggctggcg agttcgtggc ggatgctgtg aacgtttccg 1200 gtggtcgcgt gggcgaagag gttgctgtgt ggatggatct ggcttaagga tcc 1253 <210> 2 <211> 1607 <212> DNA <213> Corynebacterium glutamicum <400> 2 tctagagccg gagacgtgaa taaaattcgc agctcattcc atcagcgtaa acgcagcttt 60 ttgcatggtg agacaccttt gggggtaaat ctcacagcat gaatctctgg gttagatgac 120 tttctgggtg ggggagggtt tagaatgttt ctagtcgcac gccaaaaccc ggcgtggaca 180 cgtctgcagc cgacgcggtc gtgcctgttg tagacggaca ttcctagttt ttccaggagt 240 aacttgtgag ccagaatggc cgtccggtag tcctcatcgc cgataagctt gcgcagtcca 300 ctgttgacgc gcttggagat gcagtagaag tccgttgggt tgacggacct aaccgcccaq 360 aactgettga tgeagttaag gaageggaeg eactgetegt gegttetget accaetgteg 420

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<213> Corynebacterium glutamicum

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Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val 20 25 30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp
45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala 50 55 60

Ala Ala Pro Asn Leu Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp 65 70 75 80

Asn Val Asp Ile Pro Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn 85 90 95

Ala Pro Thr Ser Asn Ile His Ser Ala Cys Glu His Ala Ile Ser Leu

Leu Leu Ser Thr Ala Arg Gln Ile Pro Ala Ala Asp Ala Thr Leu Arg 115 120 125

Glu Gly Glu Trp Lys Arg Ser Ser Phe Asn Gly Val Glu Ile Phe Gly 130 135 140

Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala 145 150 155 160

Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
165 170 175

Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu 180 185 190

Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys 195 200 205

Thr Lys Glu Thr Ala Gly Met Phe Asp Ala Gln Leu Leu Ala Lys Ser 210 215 220

Lys Lys Gly Gln Ile Ile Ile Asn Ala Arg Gly Gly Leu Val Asp 225 230 235 240

Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala 245 250 255

Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe 260 265 270

Lys Leu Pro Gln Val Val Thr Pro His Leu Gly Ala Ser Thr Glu 275 280 285

Glu Ala Gln Asp Arg Ala Gly Thr Asp Val Ala Asp Ser Val Leu Lys 290 295 300

Ala Leu Ala Gly Glu Phe Val Ala Asp Ala Val Asn Val Ser Gly 305 310 315

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<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 12

Met Ser Gln Asn Gly Arg Pro Val Val Leu Ile Ala Asp Lys Leu Ala
1 5 10 .15

Gln Ser Thr Val Asp Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val 20 25 30

Asp Gly Pro Asn Arg Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp 35 40 45

Ala Leu Leu Val Arg Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala 50 55 60

Ala 65	Ala	Pro	Asn	Leu	Lys 70	Ile	Val	Gly	Arg	Ala 75	Gly	Val	Gly	Leu	Asp 80
Asn	Val	Asp	Ile	Pro 85	Ala	Ala	Thr	Glu	Ala 90	Gly	Val	Met	Val	Ala 95	Asn
Ala	Pro	Thr	Ser 100	Asn	Ile	His	Ser	Ala 105	Cys	Glu	His	Ala	Ile 110	Ser	Leu
Leu	Leu	Ser 115	Thr	Ala	Arg	Gln	Ile 120	Pro	Ala	Ala	Asp	Ala 125	Thr	Leu	Arg
Glu	Gly 130	Glu	Trp	Lys	Arg	Ser 135	Ser	Phe	Asn	Gly	Val 140	Glu	Ile	Phe	Gly
Lys 145	Thr	Val	Gly	Ile	Val 150	Gly	Phe	Gly	His	Ile 155	Gly	Gln	Leu	Phe	Ala 160
Gln	Arg	Leu	Ala	Ala 165	Phe	Glu	Thr	Thr	Ile 170	Val	Ala	Tyr	Asp	Pro 175	Tyr
Ala	Asn	Pro	Ala 180	Arg	Ala	Ala	Gln	Leu 185	Asn	Val	Glu	Leu	Val 190	Glu	Leu
Asp	Glu	Leu 195	Met	Ser	Arg	Ser	Asp 200	Phe	Val	Thr	Ile	His 205	Leu	Pro	Lys
Thr	Lys 210	Glu	Thr	Ala	Gly	Met 215	Phe	Asp	Ala	Gln	Leu 220	Leu	Ala	Lys	Ser
Lys 225	Lys	Gly	Gln	Ile	Ile 230	Ile	Asn	Ala	Ala	Arg 235		Gly	Leu	Val	Asp 240
Glu	Gln	Ala	Leu	Ala 245	Asp	Ala	Ile	Glu	Ser 250	Gly	His	Ile	Arg	Gly 255	Ala
Gly	Phe	Asp	Val 260	Tyr	Ser	Thr	Glu	Pro 265	Cys	Thr	Asp	Ser	Pro 270	Leu	Phe
Lys	Leu	Pro 275	Gln	Val	Val	Val	Thr 280	Pro	His	Leu	Gly	Ala 285	Ser	Thr	Glu
Glu	Ala 290	Gln	Asp	Arg	Ala	Gly 295	Thr	Asp	Val	Ala	Asp 300	Ser	Val	Leu	Lys
Ala 305	Leu	Ala	Gly	Glu	Phe 310	Val	Ala	Asp	Ala	Val 315	Asn	Val	Ser	Gly	Gly 320
Arg	Val	Gly	Glu	Glu 325	Val	Ala	Val	Trp	Met 330	Asp	Leu	Ala	Arg	Lys 335	Leu
Gly	Leu	Leu	Ala 340	Gly	Lys	Leu	Val	Asp 345	Ala	Ala	Pro	Val	Ser 350	Ile	Glu
Val	Glu	Ala 355	Arg	Gly	Glu	Leu	Ser	Ser	Glu	Gln	Val	Asp	Ala	Leu	Gly

Leu Ser Ala Val Arg Gly Leu Phe Ser Gly Ile Ile Glu Glu Ser Val

Thr Phe Val Asn Ala Pro Arg Ile Ala Glu Glu Arg Gly Leu Asp Ile

375

370

385	390	395	400
303	390	393	400

Ser Val Lys Thr Asn Ser Glu Ser Val Thr His Arg Ser Val Leu Gln 405 410 415

Val Lys Val Ile Thr Gly Ser Gly Ala Ser Ala Thr Val Val Gly Ala
420 425 430

Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile Asn Gly Arg
435 440 445

Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu Gln Tyr Thr 450 460

Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu Gly Ala Ala 465 470 475 480

Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu Lys Gly Asp 485 490 495

Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser Glu Glu Leu 500 505 510

Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe Gln Val Asp 515 520 525

Leu Asp 530

<210> 13

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

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26

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Construct

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26

<210> 15

<211> 27

<212> DNA

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ggatcc	ttac tcttcgccca cgcgacc	27
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ggatac	ctta agccagaatc catccacaca g	31
<210><211><212><212><213>	18 29 DNA Artificial Sequence	
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<210><211><211><212><213>	19 27 DNA Artificial Sequence	
<220> <223>	Description of Artificial Sequence: Synthetic Construct	
<400>	19	
ggatcct	ttaa tccaggccac ggccatt	27